(FILE 'HOME' ENTERED AT 17:07:32 ON 09 DEC 2002)

FILE 'MEDLINE, CAPLUS' ENTERED AT 17:08:02 ON 09 DEC 2002

L1	2	S (AMV OR T4 OR T7) AND (NON STANDARD NUCLEOTIDE OR NON STANDAR
L2	2	DUP REM L1 (0 DUPLICATES REMOVED)
L3	31	S (AMV OR T4 OR T7) AND (XANTHINE OR XANTHINES OR ISO C OR ISO
L4	23	DUP REM L3 (8 DUPLICATES REMOVED)
L5	4	S (AMV OR T4 OR T7) AND (AMINO ADENINE OR DEOXYXANTHOSINE OR DI
L6	3	DUP REM L5 (1 DUPLICATE REMOVED)
L7	348	S PNA AND (POLYMERASE OR POLYMERASES)
L8	197	DUP REM L7 (151 DUPLICATES REMOVED)
		E KAPLAN, B./AU
		E KAPLAN B/AU
L9	268	S E8 OR E 62 OR E63
L10	90	S E8 OR E62 OR E63
L11	59	DUP REM L10 (31 DUPLICATES REMOVED)
L12	18	S L11 AND (OLIGONUCLEOTIDE?)
		E ERITJA R/AU
L13	228	S E1 OR E4 OR E5 OR E6 OR E3
L14	156	DUP REM L13 (72 DUPLICATES REMOVED)
L15	94	S L14 AND (OLIGONUCLEOTIDE? OR POLYMERASE? OR XANTHINE OR DEOXY
L16	22	S (AMV OR T4 OR T7) AND (DEOXYINOSINE)
L17	15	DUP REM L16 (7 DUPLICATES REMOVED)
L18	78	S (AMV OR T4 OR T7) AND ("2'DEOXYINOSINE" OR INOSINE)
L19	61	DUP REM L18 (17 DUPLICATES REMOVED)
L20	51	S L19 NOT L17

L1 2 (AMV OR T4 OR T7) AND (NON STANDARD NUCLEOTIDE OR NON STANDARD BASE OR NON STANDARD NUCLEOSIDE OR NON STANDARD NUCLEOTIDES OR NON STANDARD BASES OR NON STANDARD NUCLEOSIDES)

L15 ANSWER 44 OF 94 MEDLINE
AN 89178660 MEDLINE
DN 89178660 PubMed ID: 2538629
TI Ionized and wobble base-pairing for bromouracil-guanine in equilibrium under physiological conditions. A nuclear magnetic resonance study on an **oligonucleotide** containing a bromouracil-guanine base-pair as a function of pH.
AU Sowers L C; Goodman M F; **Eritja R**; Kaplan B; Fazakerley G V
CS Department of Biological Sciences, University of Southern California, Los Angeles 90089-1481.
NC 2T32CA09320-04 (NCI)
GM21422 (NIGMS)
GM33863 (NIGMS)
SO JOURNAL OF MOLECULAR BIOLOGY, (1989 Jan 20) 205 (2) 437-47.
Journal code: 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198904
ED Entered STN: 19900306
Last Updated on STN: 19970203
Entered Medline: 19890425
AB A one and two-dimensional nuclear magnetic resonance study of a non-selfcomplementary **oligonucleotide** containing a central 5-bromouracil-guanine pair is reported. For these two bases three types of hydrogen bonding schemes could exist; wobble, rare tautomer and ionized. The two-dimensional spectra of non-exchangeable protons together with one-dimensional spectra recorded in water show that at pH 7.0 the predominant species is a right-handed B-form DNA in which the brU.G pair has wobble geometry. On raising the pH we observe a transition monitored by proton chemical shift changes for the brU.G and adjacent base-pairs. The mid-point of the transition was observed at pH 8.6. Spectra recorded at pH 9.8 show that the helix remains intact with B form conformation. It is shown that this high pH form has an ionized brU.G base-pair now in Watson-Crick geometry. Thus under physiological conditions an equilibrium exists between wobble and ionized struct

L20 ANSWER 48 OF 51 CAPLUS COPYRIGHT 2002 ACS
AN 1976:587833 CAPLUS
DN 85:187833
TI Groups on the outside of the DNA helix affect promoter utilization by **T7** RNA polymerase
AU Stahl, Stephen J.; Chamberlin, Michael J.
CS Dep. Biochem., Univ. California, Berkeley, Calif., USA
SO RNA Polym. (1976), 429-40. Editor(s): Losick, Richard; Chamberlin, Michael. Publisher: Cold Spring Harbor Lab., Cold Spring Harbor, N. Y. CODEN: 34GYA3
DT Conference
LA English
AB The utilization of a promoter site by **T7** RNA polymerase can be abolished by alterations to the DNA template nucleotides that do not alter their Watson-Crick pairing characteristics. Modified **T7** promoters were prepd. by exonuclease III degrdn. of the recombinant phage hy8 DNA, followed by repair synthesis in which one of the 4 normal deoxyribonucleoside triphosphates is replaced by a base analog-contg. nucleotide. Repair synthesis with **T7** DNA polymerase occurred only when the base analog was equiv. in pairing specificity to the missing nucleotide. The transcription pattern of modified hy8 DNA was unaffected by substitution of uracil or 5-bromouracil for thymine, whereas 5-methylcytosine or 5-hydroxymethylcytosine substituted for cytosine reduced the frequency of promoter utilization. Base analogs that alter the minor groove of the DNA helix (**inosine** for guanine, 2,6-diaminopurine for adenine) blocked the utilization of the 97% promoter by **T7** RNA polymerase. A 2nd example of the effect of residues accessible on the outside of the duplex on promoter recognition was also studied. Haemophilus aegyptius restriction endonuclease did not digest DNA with **inosine** substituted for guanine.

L6 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2002 ACS
AN 1990:454519 CAPLUS
DN 113:54519
TI Replication, transcription and nuclease digestion of the unusual X-DNA double helix of poly(amino2dA-dT)
AU Sagi, Janos; Ebinger, Katalin; Vorlickova, Michaela; Kypr, Jaroslav; Otvos, Laszlo
CS Cent. Res. Inst. Chem., Hung. Acad. Sci., Budapest, H-1525, Hung.
SO Journal of Biomolecular Structure & Dynamics (1990), 7(5), 1073-82
CODEN: JBSDD6; ISSN: 0739-1102
DT Journal
LA English
AB The alternating copolymer poly(amino2dA-dT) isomerizes into the unusual X-DNA double helix at low-salt aq. conditions. In the present paper, X-DNA replication, transcription and digestion by various polymerases and nucleases, resp., are examd. and compared to appropriate controls. X-DNA is a poor primer-template for DNA synthesis by the Escherichia coli Klenow DNA polymerase (12% of the activity obsd. with B-DNA), the Micrococcus luteus DNA polymerase I (25%) and the **AMV** reverse transcriptase (51%). In contrast, X-DNA is a better template by 74% than B-DNA for calf thymus DNA polymerase .alpha.. For transcription by E. coli RNA polymerase enzyme, poly(amino2dA-dT) did not serve as a template at all in either B or X conformation. Poly(amino2dA-dT) in its B form proved to be much more stable than poly(dA-dT) against hydrolysis by pancreatic DNase and snake venom phosphodiesterase. Formation of the X conformation in poly(amino2dA-dT) decreased this large difference in nuclease stability.